

RESULT 1  
 US-09-818-780-89  
 ; Sequence 89, Application US/09818780  
 ; Patent No. 6677146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McHenry, Charles  
 ; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME  
 ; FILE REFERENCE: 1794.0030004  
 ; CURRENT APPLICATION NUMBER: US/09/818,780  
 ; CURRENT FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/192,736  
 ; PRIOR FILING DATE: 2000-03-28  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 89  
 ; LENGTH: 305  
 ; TYPE: PRT  
 ; ORGANISM: Aquifex aeolicus  
 US-09-818-780-89

Query Match 100.0%; Score 1570; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-142;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV	120
Qy	121	KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV	180
Db	121	KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV	180
Qy	181	EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS	240
Db	181	EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS	240
Qy	241	EFEKWEPEKQKLFLEIMEELVSQKLTEEKKNYTYLLDTIRLFKDGGLARGVNEPLWLFTL	300
Db	241	EFEKWEPEKQKLFLEIMEELVSQKLTEEKKNYTYLLDTIRLFKDGGLARGVNEPLWLFTL	300
Qy	301	AVQAD	305
Db	301	AVQAD	305

RESULT 1  
 D70432  
 conserved hypothetical protein aq\_1526 - Aquifex aeolicus  
 C;Species: Aquifex aeolicus  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C;Accession: D70432

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: D70432  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-305  
 A;Cross-references: UNIPROT:O67486; UNIPARC:UPI000004350C; GB:AE000744; NID:g2983891; PIDN:AAC07454.1; PID:g2983903; GB:AE000657  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: aq\_1526

Query Match 100.0%; Score 1570; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-92;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTKTAFEFAGKILCKENVPWGCSCPSCKHVN 60
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Db      1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTKTAFEFAGKILCKENVPWGCSCPSCKHVN 60

Qy     61 ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120

Qy    121 KPALSRRKVIIIDAHAMTSQAANALLKVLEEPADTTFILTTNRRSAILPTILSRTFQV 180
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Db    121 KPALSRRKVIIIDAHAMTSQAANALLKVLEEPADTTFILTTNRRSAILPTILSRTFQV 180

Qy    181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS 240
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Db    181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS 240

Qy    241 EFKEWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300
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Db    301 AVQAD 305

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RESULT 1  
 O67486\_AQUAE  
 ID O67486\_AQUAE PRELIMINARY; PRT; 305 AA.  
 AC O67486;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein aq\_1526.  
 GN OrderedLocusNames=AQ\_1526;  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OX NCBI\_TaxID=63363;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000744; AAC07454.1; -; Genomic\_DNA.  
 DR PIR; D70432; D70432.  
 DR HSSP; P06710; 1NJF.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR SMART; SM00382; AAA; 1.  
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
 SQ SEQUENCE 305 AA; 34897 MW; 2B207935455B7E8A CRC64;

Query Match 100.0%; Score 1570; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-91;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEKVFLEKLQKTLHIPGGLLFYKGEGSGKTKTAFEFAKGILCKENVPWGCSCPSCKHVN	60
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Qy	61	ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV	120
Db	61	ELEEAFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV	120
Qy	121	KPALSRRKVIIIDDAHAMTSQAANALLKVLEPPADTTFILTTNRRSAILPTILSRTFQV	180
Db	121	KPALSRRKVIIIDDAHAMTSQAANALLKVLEPPADTTFILTTNRRSAILPTILSRTFQV	180
Qy	181	EFKGFVSKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS	240
Db	181	EFKGFVSKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLAS	240
Qy	241	EFEKWEPEKQKLFLEIMEELVSQKLTEEEKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL	300
Db	241	EFEKWEPEKQKLFLEIMEELVSQKLTEEEKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL	300
Qy	301	AVQAD	305
Db	301	AVQAD	305

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:57:48 ON 01 DEC 2008)

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOTECHNO, EMBASE, JAPIO' ENTERED AT  
15:00:53 ON 01 DEC 2008

L1            217 S AQUIFEX AND POLYMERASE  
L2            110 DUP REM L1 (107 DUPLICATES REMOVED)  
L3            9 S L2 AND DELTA